IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN RE PATENT APPLICATION OF

HARBERD et al   Atty. Ref.:   620-157

Serial No.:   09/911,513   Group Art Unit: 1638

Filed: July 25, 2001   Examiner: Mehta, A.

For: NUCLEIC ACID ENCODING GAI GENE OF ARABIDOPSIS THALIANA

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December 19, 2002

SUBMISSION OF FORMAL DRAWINGS

Hon. Commissioner of Patents
  and Trademarks
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Attn: Official Draftsperson

Sir:

Enclosed herewith are 13 sheets of formal, inked

drawings for the above-identified application.

Respectfully submitted,

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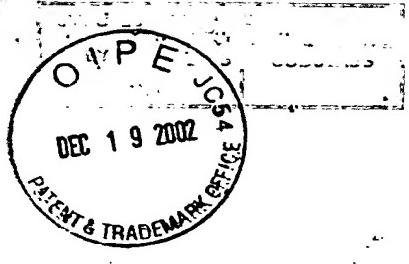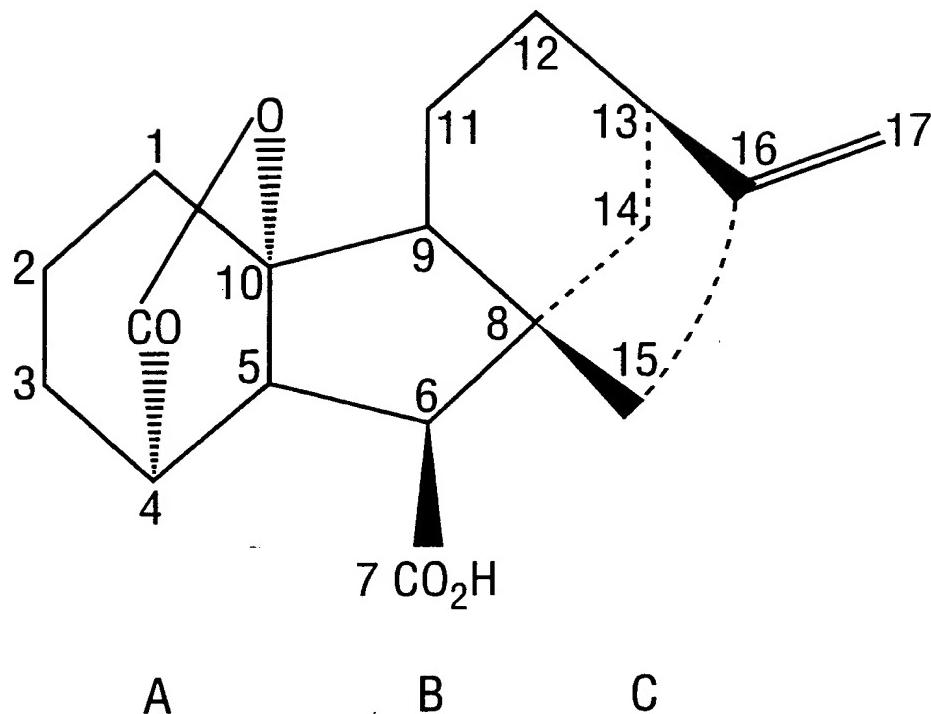
FIG. 1

A   B   C

FIG. 2a

FIG. 2b

GAI   gai   gai-t6

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FIG. 2c

GAI   gai   gai-t6

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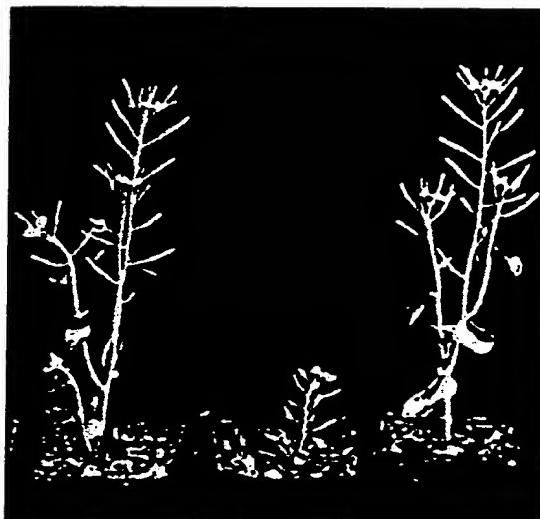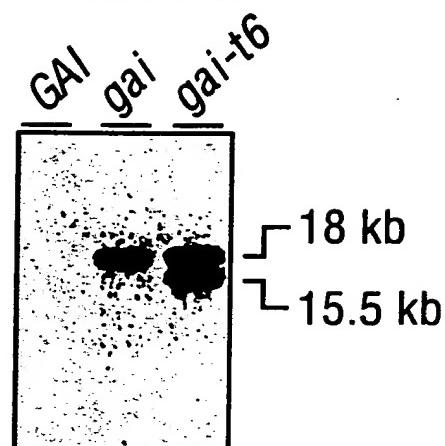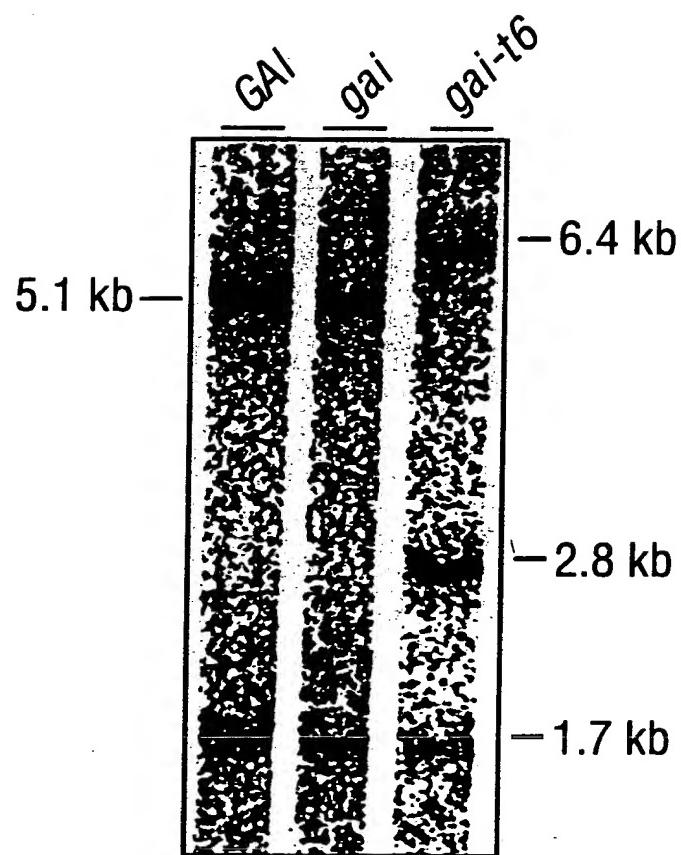
Figure 3

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TAATAATCAT TTTTTTTCTT ATAACCTTCC TCTCTATTTT TACAATTTAT TTTGTTATTA      60
GAAGTGGTAG TGGAGTGAAA AAACAAATCC TAAGCAGTCC TAACCGATCC CCGAAGCTAA     120
AGATTCTTCA CCTTCCCAAA TAAAGCAAAA CCTAGATCCG ACATTGAAGG AAAAACCTTT     180
TAGATCCATC TCTGAAAAAA AACCAACCAT GAAGAGAGAT CATCATCATC ATCATCAAGA     240
TAAGAAGACT ATGATGATGA ATGAAGAAGA CGACGGTAAC GGCATGGATG AGCTTCTAGC     300
TGTTCTTGGT TACAAGGTTA GGTCATCGGA AATGGCTGAT GTTGCTCAGA AACTCGAGCA     360
GCTTGAAGTT ATGATGTCTA ATGTTCAAGA AGACGATCTT TCTCAACTCG CTACTGAGAC     420
TGTTCACTAT AATCCGGCGG AGCTTTACAC GTGGCTTGAT TCTATGCTCA CCGACCTTAA     480
TCCTCCGTCG TCTAACGCCG AGTACGATCT TAAAGCTATT CCCGGTGACG CGATTCTCAA     540
TCAGTTCGCT ATCGATTCGG CTTCTTCGTC TAACCAAGGC GGCGGAGGAG ATACGTATAC     600
TACAAACAAG CGGTTGAAAT GCTCAAACGG CGTCGTGGAA ACCACCACAG CGACGGCTGA     660
GTCAACTCGG CATGTTGTCC TGGTTGACTC GCAGGAGAAC GGTGTGCGTC TCGTTCACGC     720
GCTTTTGGCT TGCGCTGAAG CTGTTCAGAA GGAGAATCTG ACTGTGGCGG AAGCTCTGGT     780
GAAGCAAATC GGATTCTTAG CTGTTTCTCA AATCGGAGCT ATGAGAAAAG TCGCTACTTA     840
CTTCGCCGAA GCTCTCGCGC GGCGGATTTA CCGTCTCTCT CCGTCGCAGA GTCCAATCGA     900
CCACTCTCTC TCCGATACTC TTCAGATGCA CTTCTACGAG ACTTGTCCTT ATCTCAAGTT     960
CGCTCACTTC ACGGCGAATC AAGCGATTCT CGAAGCTTTT CAAGGGAAGA AAGAGTTCA    1020
TGTCATTGAT TTCTCTATGA GTCAAGGTCT TCAATGGCCG GCGCTTATGC AGGCTCTTGC    1080
GCTTCGACCT GGTGGTCCTC CTGTTTTCCG GTTAACCGGA ATTGGTCCAC CGGCACCGGA    1140
TAATTTCGAT TATCTTCATG AAGTTGGGTG TAAGCTGGCT CATTTAGCTG AGGCGATTCA    1200
CGTTGAGTTT GAGTACAGAG GATTTGTGGC TAACACTTTA GCTGATCTTG ATGCTTCGAT    1260
GCTTGAGCTT AGACCAAGTG AGATTGAATC TGTTGCGGTT AACTCTGTTT TCGAGCTTCA    1320
CAAGCTCTTG GGACGACCTG GTGCGATCGA TAAGGTTCTT GGTGTGGTGA ATCAGATTAA    1380
ACCGGAGATT TTCACTGTGG TTGAGCAGGA ATCGAACCAT AATAGTCCGA TTTTCTTAGA    1440
TCGGTTTACT GAGTCGTTGC ATTATTACTC GACGTTGTTT GACTCGTTGG AAGGTGTACC    1500
GAGTGGTCAA GACAAGGTCA TGTCGGAGGT TTACTTGGGT AAACAGATCT GCAACGTTGT    1560
GGCTTGTGAT GGACCTGACC GAGTTGAGCG TCATGAAACG TTGAGTCAGT GGAGGAACCG    1620
GTTCGGGTCT GCTGGGTTTG CGGCTGCACA TATTGGTTCG AATGCGTTTA AGCAAGCGAG    1680
TATGCTTTTG GCTCTGTTCA ACGGCGGTGA GGGTTATCGG GTGGAGGAGA GTGACGGCTG    1740
TCTCATGTTG GGTTGGCACA CACGACCGCT CATAGCCACC TCGGCTTGGA AACTCTCCAC    1800
CAATTAGATG GTGGCTCAAT GAATTGATCT GTTGAACCGG TTATGATGAT AGATTTCCGA    1860
CCGAAGCCAA ACTAAATCCT ACTGTTTTTC CCTTTGTCAC TTGTTAAGAT CTTATCTTTC    1920
ATTATATTAG GTAATTGAAA AATTTCTAAA TTACTCACAC TGGC                     1964
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Figure 4

```
MetLysArgAspHisHisHisHisHisGlnAspLysLysThrMetMetMetAsnGluGlu        20

AspAspGlyAsnGlyMetAspGluLeuLeuAlaValLeuGlyTyrLysValArgSerSer        40

GluMetAlaAspValAlaGlnLysLeuGluGlnLeuGluValMetMetSerAsnValGln        60

GluAspAspLeuSerGlnLeuAlaThrGluThrValHisTyrAsnProAlaGluLeuTyr        80

ThrTrpLeuAspSerMetLeuThrAspLeuAsnProProSerSerAsnAlaGluTyrAsp       100

LeuLysAlaIleProGlyAspAlaIleLeuAsnGlnPheAlaIleAspSerAlaSerSer       120

SerAsnGlnGlyGlyGlyGlyAspThrTyrThrThrAsnLysArgLeuLysCysSerAsn       140

GlyValValGluThrThrThrAlaThrAlaGluSerThrArgHisValValLeuValAsp       160

SerGlnGluAsnGlyValArgLeuValHisAlaLeuLeuAlaCysAlaGluAlaValGln       180

LysGluAsnLeuThrValAlaGluAlaLeuValLysGlnIleGlyPheLeuAlaValSer       200

GlnIleGlyAlaMetArgLysValAlaThrTyrPheAlaGluAlaLeuAlaArgArgIle       220

TyrArgLeuSerProSerGlnSerProIleAspHisSerLeuSerAspThrLeuGlnMet       240

HisPheTyrGluThrCysProTyrLeuLysPheAlaHisPheThrAlaAsnGlnAlaIle       260

LeuGluAlaPheGlnGlyLysLysArgValHisValIleAspPheSerMetSerGlnGly       280

LeuGlnTrpProAlaLeuMetGlnAlaLeuAlaLeuArgProGlyGlyProProValPhe       300

ArgLeuThrGlyIleGlyProProAlaProAspAsnPheAspTyrLeuHisGluValGly       320

CysLysLeuAlaHisLeuAlaGluAlaIleHisValGluPheGluTyrArgGlyPheVal       340

AlaAsnThrLeuAlaAspLeuAspAlaSerMetLeuGluLeuArgProSerGluIleGlu       360

SerValAlaValAsnSerValPheGluLeuHisLysLeuLeuGlyArgProGlyAlaIle       380

AspLysValLeuGlyValValAsnGlnIleLysProGluIlePheThrValValGluGln       400

GluSerAsnHisAsnSerProIlePheLeuAspArgPheThrGluSerLeuHisTyrTyr       420

SerThrLeuPheAspSerLeuGluGlyValProSerGlyGlnAspLysValMetSerGlu       440

ValTyrLeuGlyLysGlnIleCysAsnValValAlaCysAspGlyProAspArgValGlu       460

ArgHisGluThrLeuSerGlnTrpArgAsnArgPheGlySerAlaGlyPheAlaAlaAla       480

HisIleGlySerAsnAlaPheLysGlnAlaSerMetLeuLeuAlaLeuPheAsnGlyGly       500

GluGlyTyrArgValGluGluSerAspGlyCysLeuMetLeuGlyTrpHisThrArgPro       520

LeuIleAlaThrSerAlaTrpLysLeuSerThrAsn                               532
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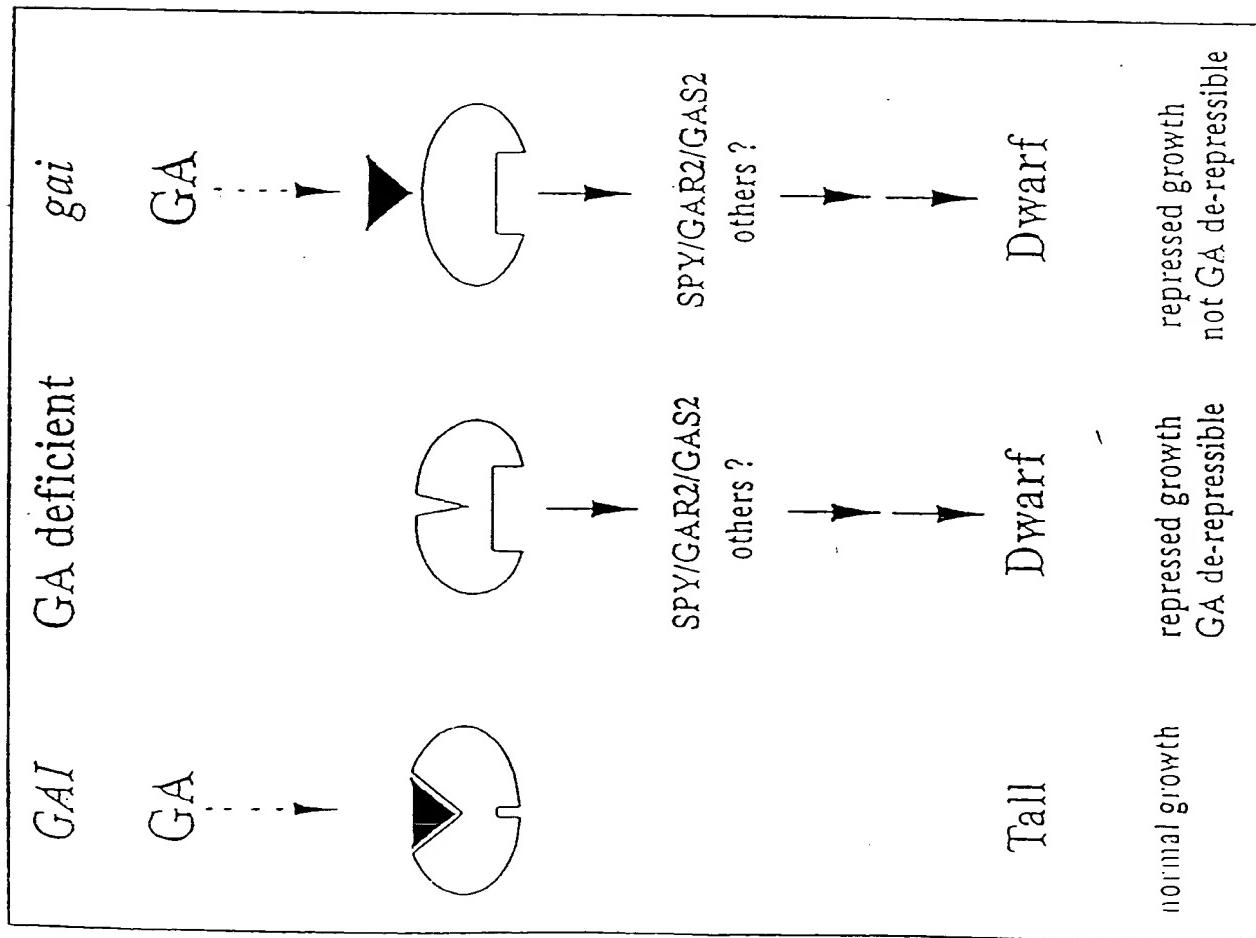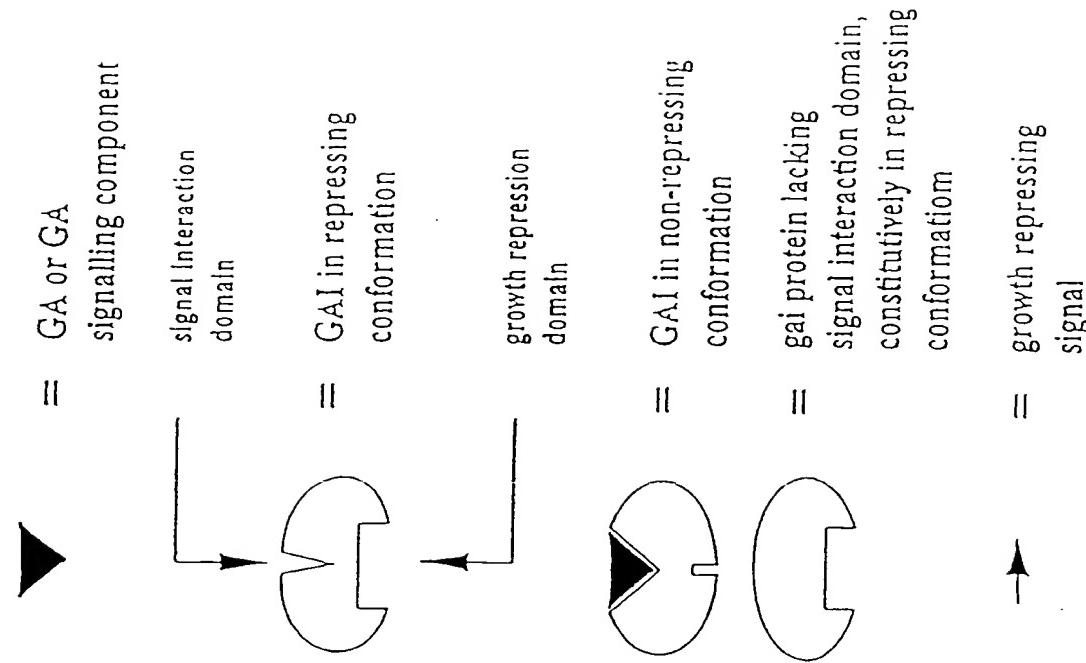
Figure 5

Figure 6(a)

```
   1   TAGAAGTGGT AGTCGAGTGA AAAAACAAAT CCTAAGCAGT CCTAACCGAT

  51   CCCCGAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC

 101   CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC

 151   ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT

 201   GAATGAAGAA GACGACGGTA ACGGCATGGA TGTTGCTCAG AAACTCGAGC

 251   AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC

 301   GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTTACA CGTGGCTTGA

 351   TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC

 401   TTAAAGCTAT TCCCGGTGAC GCGATTCTCA ATCAGTTCGC TATCGATTCG

 451   GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACGTATA CTACAAACAA

 501   GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCACCACA GCGACGGCTG

 551   AGTCAACTCG GCATGTTGTC CTGGTTGACT CGCAGGAGAA CGGTGTGCGT

 601   CTCGTTCACG CGCTTTTGGC TTGCGCTGAA GCTGTTCAGA AGGAGAATCT

 651   GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTTCTC

 701   AAATCGGAGC TATGAGAAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGCG

 751   CGGCGGATTT ACCGTCTCTC TCCGTCGCAG AGTCCAATCG ACCACTCTCT

 801   CTCCGATACT CTTTAGATGC ACTTCTACGA GACTTGTCCT TATCTCAAGT

 851   TCGCTCACTT CACGGCGAAT CAAGCGATTC TCGAAGCTTT TCAAGGGAAG

 901   AAAAGAGTTC ATGTCATTGA TTTCTCTATG AGTCAAGGTC TTCAATGGCC

 951   GGCGCTTATG CAGGCTCTTG CGCTTCGACC TGGTGGTCCT CCTGTTTTCC

1001   GGTTAACCGG AATTGGTCCA CCGGCACCGG ATAATTTCGA TTATCTTCAT

1051   GAAGTTGGGT GTAAGCTGGC TCATTTAGCT GAGGCGATTC ACGTTGAGTT

1101   TGAGTACAGA GGATTTGTGG CTAACACTTT AGCTGATCTT GATGCTTCGA

1151   TGCTTGAGCT TAGACCAAGT GAGATTGAAT CTGTTGCGGT TAACTCTGTT

1201   TTCGAGCTTC ACAAGCTCTT GGGACGACCT GGTGCGATCG ATAAGGTTCT

1251   TGGTGTGGTG AATCAGATTA AACCGGAGAT TTTCACTGTG GTTGAGCAGG

1301   AATCGAACCA TAATAGTCCG ATTTTCTTAG ATCGGTTTAC TGAGTCGTTG

1351   CATTATTACT CGACGTTGTT TGACTCGTTG GAAGGTGTAC CGAGTGGTCA

1401   AGACAAGGTC ATGTCGGAGG TTTACTTGGG TAAACAGATC TGCAACGTTG

1451   TGGCTTGTGA TGGACCTGAC CGAGTTGAGC GTCATGAAAC GTTGAGTCAG

1501   TGGAGGAACC GGTTCGGGTC TGCTGGGTTT GCGGCTGCAC ATATTGGTTC

1551   GAATGCGTTT AAGCAAGCGA GTATGCTTTT GGCTCTGTTC AACGGCGGTG

1601   AGGGTTATCG GGTGGAGGAG AGTGACGGCT GTCTCATGTT GGG
```

Figure 6(b)

```
  1    MKRDHHHHHQ DKKTMMMNEE DDGNGMDVAQ KLEQLEVMMS NVQEDDLSQL

 51    ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS

101    ASSSNQGGGG DTYTTNKRLK CSNGVVETTT ATAESTRHVV LVDSQENGVR

151    LVHALLACAE AVQKENLTVA EALVKQIGFL AVSQIGAMRK VATYFAEALA

201    RRIYRLSPSQ SPIDHSLSDT L*
```

Figure 6(c)

```
   1  TAGAAGTGGT AGTGGAGTGA AAAAACAAAT CCTAAGCAGT CCTAACCGAT
  51  CCCCGAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
 101  CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
 151  ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
 201  GAATGAAGAA GACGACGGTA ACGGCATGGA TGTTGCTCAG AAACTCGAGC
 251  AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
 301  GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTTACA CGTGGCTTGA
 351  TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
 401  TTAAAGCTAT TCCCGGTGAC GCGATTCTCA ATCAGTTCGC TATCGATTCG
 451  GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACGTATA CTACAAACAA
 501  GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCACCACA GCGACGGCTG
 551  AGTCAACTCG GCATGTTGTC CTGGTTGACT CGCAGGAGAA CGGTGTGCGT
 601  CTCGTTCACG CGCTTTTGGC TTGCGCTGAA GCTGTTCAGA AGGAGAATCT
 651  GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTTCTC
 701  AAATCGGAGC TATGAGAAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGCG
 751  CGGCGGATTT ACCGTCTCTC TCCGTCGCAG AGTCCAATCG ACCACTCTCT
 801  CTCCGATACT CTTCAGATGC ACTTCTACGA GACTTGTCCT TATCTCAAGT
 851  TCGCTCACTT CACGGCGAAT CAAGCGATTC TCGAAGCTTT TCAAGGGAAG
 901  AAAAGAGTTC ATGTCATTGA TTCTCTATGA GTCAAGGTCT TCAATGGCCG
 951  GCGCTTATGC AGGCTCTTGC GCTTCGACCT GGTGGTCCTC CTGTTTTCCG
1001  GTTAACCGGA ATTGGTCCAC CGGCACCGGA TAATTTCGAT TATCTTCATG
1051  AAGTTGGGTG TAAGCTGGCT CATTTAGCTG AGGCGATTCA CGTTGAGTTT
1101  GAGTACAGAG GATTTGTGGC TAACACTTTA GCTGATCTTG ATGCTTCGAT
1151  GCTTGAGCTT AGACCAAGTG AGATTGAATC TGTTGCGGTT AACTCTGTTT
1201  TCGAGCTTCA CAAGCTCTTG GGACGACCTG GTGCGATCGA TAAGGTTCTT
1251  GGTGTGGTGA ATCAGATTAA ACCGGAGATT TTCACTGTGG TTGAGCAGGA
1301  ATCGAACCAT AATAGTCCGA TTTTCTTAGA TCGGTTTACT GAGTCGTTGC
1351  ATTATTACTC GACGTTGTTT GACTCGTTGG AAGGTGTACC GAGTGGTCAA
1401  GACAAGGTCA TGTCGGAGGT TTACTTGGGT AAACAGATCT GCAACGTTGT
1451  GGCTTGTGAT GGACCTGACC GAGTTGAGCG TCATGAAACG TTGAGTCAGT
1501  GGAGGAACCG GTTCGGGTCT GCTGGGTTTG CGGCTGCACA TATTGGTTCG
1551  AATGCGTTTA AGCAAGCGAG TATGCTTTTG GCTCTGTTCA ACGGCGGTGA
1601  GGGTTATCGG GTGGAGGAGA GTGACGGCTG TCTCATGTTG GG
```

Figure 6(d)

```
  1   MKRDHHHHHQ  DKKTMMMNEE  DDGNGMDVAQ  KLEQLEVMMS  NVQEDDLSQL

 51   ATETVHYNPA  ELYTWLDSML  TDLNPPSSNA  EYDLKAIPGD  AILNQFAIDS

101   ASSSNQGGGG  DTYTTNKRLK  CSNGVVETTT  ATAESTRHVV  LVDSQENGVR

151   LVHALLACAE  AVQKENLTVA  EALVKQIGFL  AVSQIGAMRK  VATYFAEALA

201   RRIYRLSPSQ  SPIDHSLSDT  LQMHFYETCP  YLKFAHFTAN  QAILEAFQGK

251   KRVHVIDSL*
```

Figure 6(e)

```
   1   TAGAAGTGGT AGTGGAGTGA AAAAACAAAT CCTAAGCAGT CCTAACCGAT
  51   CCCCGAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
 101   CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
 151   ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
 201   GAATGAAGAA GACGACGGTA ACGGCATGGA TGTTGCTCAG AAACTCGAGC
 251   AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
 301   GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTTACA CGTGGCTTGA
 351   TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
 401   TTAAAGCTAT TCCCGGTGAC GCGATTCTCA ATCAGTTCGC TATCGATTCG
 451   GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACGTATA CTACAAACAA
 501   GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCACCACA GCGACGGCTG
 551   AGTCAACTCG GCATGTTGTC CTGGTTGACT CGCAGGAGAA CGGTGTGCGT
 601   CTCGTTCACG CGCTTTTGGC TTGCGCTGAA GCTGTTCAGA AGGAGAATCT
 651   GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTTCTC
 701   AAATCGGAGC TATGAGAAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGCG
 751   CGGCGGATTT ACCGTCTCTC TCCGTCGCAG AGTCCAATCG ACCACTCTCT
 801   CTCCGATACT CTTCAGATGC ACTTCTACGA GACTTGTCCT TATCTCAAGT
 851   TCGCTCACTT CACGGCGAAT CAAGCGATTC TCGAAGCTTT TCAAGGGAAG
 901   AAAAGAGTTC ATGTCATTGA TTTCTCTATG AGTCAAGGTC TTGGGCGCTT
 951   ATGCAGGCTC TTGCGCTTCG ACCTGGTGGT CCTCCTGTTT TCCGGTTAAC
1001   CGGAATTGGT CCACCGGCAC CGGATAATTT CGATTATCTT CATGAAGTTG
1051   GGTGTAAGCT GGCTCATTTA GCTGAGGCGA TTCACGTTGA GTTTGAGTAC
1101   AGAGGATTTG TGGCTAACAC TTTAGCTGAT CTTGATGCTT CGATGCTTGA
1151   GCTTAGACCA AGTGAGATTG AATCTGTTGC GGTTAACTCT GTTTTCGAGC
1201   TTCACAAGCT CTTGGGACGA CCTGGTGCGA TCGATAAGGT TCTTGGTGTG
1251   GTGAATCAGA TTAAACCGGA GATTTTCACT GTGGTTGAGC AGGAATCGAA
1301   CCATAATAGT CCGATTTTCT TAGATCGGTT TACTGAGTCG TTGCATTATT
1351   ACTCGACGTT GTTTGACTCG TTGGAAGGTG TACCGAGTGG TCAAGACAAG
1401   GTCATGTCGG AGGTTTACTT GGGTAAACAG ATCTGCAACG TTGTGGCTTG
1451   TGATGGACCT GACCGAGTTG AGCGTCATGA AACGTTGAGT CAGTGGAGGA
1501   ACCGGTTCGG GTCTGCTGGG TTTGCGGCTG CACATATTGG TTCGAATGCG
1551   TTTAAGCAAG CGAGTATGCT TTTGGCTCTG TTCAACGGCG GTGAGGGTTA
1601   TCGGGTGGAG GAGAGTGACG GCTGTCTCAT GTTGGG
```

Figure 6(f)

```
  1   MKRDHHHHHQ DKKTMMMNEE DDGNGMDVAQ KLEQLEVMMS NVQEDDLSQL

 51   ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS

101   ASSSNQGGGG DTYTTNKRLK CSNGVVETTT ATAESTRHVV LVDSQENGVR

151   LVHALLACAE AVQKENLTVA EALVKQIGFL AVSQIGAMRK VATYFAEALA

201   RRIYRLSPSQ SPIDHSLSDT LQMHFYETCP YLKFAHFTAN QAILEAFQGK

251   KRVHVIDFSM SQGLGRLCRL LRFDLVVLLF SG*
```

Figure 6(g)

```
   1   TAGAAGTGGT AGTGGAGTGA AAAAACAAAT CCTAAGCAGT CCTAACCGAT
  51   CCCCGAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
 101   CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
 151   ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
 201   GAATGAAGAA GACGACGGTA ACGGCATGGA TGTTGCTCAG AAACTCGAGC
 251   AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
 301   GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTTACA CGTGGCTTGA
 351   TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
 401   TTAAAGCTAT TCCCGGTGAC GCGATTCTCA ATCAGTTCGC TATCGATTCG
 451   GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACGTATA CTACAAACAA
 501   GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCACCACA GCGACGGCTG
 551   AGTCAACTCG GCATGTGTCC TGGTTGACTC GCAGGAGAAC GGTGTGCGTC
 601   TCGTTCACGC GCTTTTGGCT TGCGCTGAAG CTGTTCAGAA GGAGAATCTG
 651   ACTGTGGCGG AAGCTCTGGT GAAGCAAATC GGATTCTTAG CTGTTTCTCA
 701   AATCGGAGCT ATGAGAAAAG TCGCTACTTA CTTCGCCGAA GCTCTCGCGC
 751   GGCGGATTTA CCGTCTCTCT CCGTCGCAGA GTCCAATCGA CCACTCTCTC
 801   TCCGATACTC TTCAGATGCA CTTCTACGAG ACTTGTCCTT ATCTCAAGTT
 851   CGCTCACTTC ACGGCGAATC AAGCGATTCT CGAAGCTTTT CAAGGGAAGA
 901   AAAGAGTTCA TGTCATTGAT TTCTCTATGA GTCAAGGTCT TCAATGGCCG
 951   GCGCTTATGC AGGCTCTTGC GCTTCGACCT GGTGGTCCTC CTGTTTTCCG
1001   GTTAACCGGA ATTGGTCCAC CGGCACCGGA TAATTTCGAT TATCTTCATG
1051   AAGTTGGGTG TAAGCTGGCT CATTTAGCTG AGGCGATTCA CGTTGAGTTT
1101   GAGTACAGAG GATTTGTGGC TAACACTTTA GCTGATCTTG ATGCTTCGAT
1151   GCTTGAGCTT AGACCAAGTG AGATTGAATC TGTTGCGGTT AACTCTGTTT
1201   TCGAGCTTCA CAAGCTCTTG GGACGACCTG GTGCGATCGA TAAGGTTCTT
1251   GGTGTGGTGA ATCAGATTAA ACCGGAGATT TTCACTGTGG TTGAGCAGGA
1301   ATCGAACCAT AATAGTCCGA TTTTCTTAGA TCGGTTTACT GAGTCGTTGC
1351   ATTATTACTC GACGTTGTTT GACTCGTTGG AAGGTGTACC GAGTGGTCAA
1401   GACAAGGTCA TGTCGGAGGT TTACTTGGGT AAACAGATCT GCAACGTTGT
1451   GGCTTGTGAT GGACCTGACC GAGTTGAGCG TCATGAAACG TTGAGTCAGT
1501   GGAGGAACCG GTTCGGGTCT GCTGGGTTTG CGGCTGCACA TATTGGTTCG
1551   AATGCGTTTA AGCAAGCGAG TATGCTTTTG GCTCTGTTCA ACGGCGGTGA
1601   GGGTTATCGG GTGGAGGAGA GTGACGGCTG TCTCATGTTG GG
```

Figure 6(h)

```
  1  MKRDHHHHHQ DKKTMMMNEE DDGNGMDVAQ KLEQLEVMMS NVQEDDLSQL

 51  ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS

101  ASSSNQGGGG DTYTTNKRLK CSNGVVETTT ATAESTRHVS WLTRRRTVCV

151  SFTRFWLALK LFRRRI*
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